set of nucleic acids, comprising:

a) generating random oligonucleotides, wherein said oligonucleotides are of a uniform length comprising a single stranded, central segment of randomly varied bases and flanking segments of defined sequences on each side of said central segment;

b) hybridizing the random oligonucleotides with a nucleic acid-containing template of biological or synthetic origin under hybridization conditions that enable the formation of duplexes and using blockers to avoid hybridization of said flanking segments;

c) eliminating non-specific duplexes using conditions that minimize or abrogate mismatches;

d) separating the hybridized oligonucleotides from the duplexes obtained in step c); and

e) amplifying the hybridized oligonucleotides.

2. (Amended) A process as defined in claim 1, further comprising subtracting between two different oligonucleotide libraries (OL1 and OL2) which contain similar sequence motifs.

3. (Amended) A process as defined in claim 2, wherein said subtracting comprises:

a) generating single stranded versions of OL1 and OL2;

b) annealing the OL1 strands with an excess of OL2 strands, under hybridization conditions;

c) partitioning double stranded hybrids (OL1:OL2) and single stranded OL2 from single stranded OL1;

d) amplifying the single stranded OL1; and

e) repeating steps a) to d) to obtain OL1 oligonucleotides with reduced affinity for OL2.

A1

4. (Amended) A process as defined in claim 1, wherein said central segment comprises 10-40 bases and each one of said flanking segments comprises 10-40 bases.

A2

6. (Amended) A process as defined in claim 1, wherein the nucleic acid-containing template comprises at least one of genomic or synthetic DNA or RNA, or cDNA.

8. (Amended) A library of oligonucleotides produced by the process comprising:

A3

a) generating random oligonucleotides, wherein said oligonucleotides are of a uniform length comprising a single stranded, central segment of randomly varied bases and flanking segments of defined sequences on each side of said central segment;

b) hybridizing the random oligonucleotides with a nucleic acid-containing template of biological or synthetic origin under hybridization conditions that enable the formation of duplexes and using blockers to avoid hybridization of said flanking segments;

c) eliminating non-specific duplexes using conditions that minimize or abrogate mismatches;

d) separating the hybridized oligonucleotides from the duplexes obtained in step c); and

e) amplifying the hybridized oligonucleotides.

9. (Amended) Use of a library of oligonucleotides produced by the process of claim 1 in a diagnostic kit.

10. (Amended) Use of a library of oligonucleotides produced by the process of claim 1 to inhibit gene function.

11. (Amended) A method of diagnosis comprising use of a library of oligonucleotides produced by the process of claim 1.

12. (Amended) Use of a library of oligonucleotides produced by the process of claim 1 wherein said oligonucleotides are bound to a solid support.

13. (Amended) A use as defined in claim 12, wherein the solid support is at least one of a membrane, glass slide, coated glass slide, printed arrays, microspheres or chromatographic media.

14. (Amended) Use of a library of oligonucleotides produced by the process of claim 1, wherein said oligonucleotides are hybridized to nucleic acid arrays.